SEQUENCE LISTING

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<120>	IDENTIFICATION AND MODULATION OF A G-PROTEIN COUPLED RECEPTOR (GPCR), RAI3, ASSOCIATED WITH CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD) AND NF-kB AND E-SELECTIN REGULATION	8
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Thr	Val	Ala 35	Thr	Ala	Gly	Val	Val 40	Thr	Ser	Val	Ala	Phe 45	Met	Leu	Thr
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Leu	Thr	Phe	Ala	Phe 85	Ile	Ile	Gly	Leu	Asp 90	Gly	Ser	Thr	Gly	Pro 95	Thr
Arg	Phe	Phe	Leu 100	Phe	Gly	Ile	Leu	Phe 105	Ser	Ile	Cys	Phe	Ser 110	Cys	Leu
Leu	Ala	His 115	Ala	Val	Ser	Leu	Thr 120	Lys	Leu	Val	Arg	Gly 125	Arg	Lys	Pro
Leu	Ser 130	Leu	Leu	Val	Ile	Leu 135	Gly	Leu	Ala	Val	Gly 140	Phe	Ser	Leu	Val
Gln 145	Asp	Val	Ile	Ala	Ile 150	Glu	Tyr	Ile	Val	Leu 155	Thr	Met	Asn	Arg	Thr 160

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Phe Val Leu Leu Thr Tyr Val Leu Phe Leu Met Ala Leu Thr Phe
180 185 190

Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg
195 200 205

His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp 210 215 220

Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp 225 230 235 240

Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe 245 250 255

Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg
260 265 270

Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu 275 280 285

Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu 290 295 300

Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr 305 310 315 320

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<213> Homo sapiens

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Leu Arg Gly Asn Pro Gln Phe Gln Arg Gln Pro Gln Trp Asp Asp Pro 225 230 235 240

Thr Val Leu Phe Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu

200

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Val Val Cys Ile Ala Leu Val Thr Asn Ala Trp Val Phe Leu Leu Leu 245 250 255

Tyr Ile Val Pro Glu Leu Cys Ile Leu Tyr Arg Ser Cys Arg Gln Glu 260 265 270

Cys Pro Leu Gln Gly Asn Ala Cys Pro Val Thr Ala Tyr Gln His Ser 275 280 285

Phe Gln Val Glu Asn Gln Glu Leu Ser Arg Ala Arg Asp Ser Asp Gly 290 295 300

Ala Glu Glu Asp Val Ala Leu Thr Ser Tyr Gly Thr Pro Ile Gln Pro 305 310 315 320

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Arg Lys Val Gln Asp Cys Ser Gln Trp Asn Val Leu Pro Thr Gln Phe 50 60

Leu Phe Leu Leu Ala Val Leu Gly Leu Phe Gly Leu Thr Phe Ala Phe 65 70 75 80

Ile Ile Gln Leu Asn His Gln Thr Ala Pro Val Arg Tyr Phe Leu Phe

90 95

Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Leu Ala His Ala Ser 100 105 110

Asn Leu Val Lys Leu Val Arg Gly Arg Val Ser Phe Cys Trp Thr Thr 115 120 125

Ile Leu Phe Ile Ala Ile Gly Val Ser Leu Leu Gln Thr Ile Ile Ala 130 135 140

Ile Glu Tyr Val Thr Leu Ile Met Thr Arg Gly Leu Met Phe Glu His 145 (150 155 160

Met Thr Pro Tyr Gln Leu Asn Val Asp Phe Val Cys Leu Leu Ile Tyr 165 170 175

Val Leu Phe Leu Met Ala Leu Thr Phe Phe Val Ser Lys Ala Thr Phe 180 185 190

Cys Gly Pro Cys Glu Asn Trp Lys Gln His Gly Arg Leu Ile Phe Ala 195 200 205

Thr Val Leu Val Ser Ile Ile Ile Trp Val Val Trp Ile Ser Met Leu 210 215 220

Leu Arg Gly Asn Pro Gln Leu Gln Arg Gln Pro His Trp Asp Asp Ala 225 230 235 240

Val Ile Cys Ile Gly Leu Val Thr Asn Ala Trp Val Phe Leu Leu Ile 245 250 255

Tyr Ile Ile Pro Glu Leu Ser Ile Leu Tyr Arg Ser Cys Arg Gln Glu 260 265 270

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Cys Asp Leu Asp Ala Ile Trp Gly Ile Val Val Glu Ala Val Ala Gly 50 55 60

Ala Gly Ala Leu Ile Thr Leu Leu Met Leu Ile Leu Leu Val Arg 65 70 75 80

Leu Pro Phe Ile Lys Glu Lys Glu Lys Ser Pro Val Gly Leu His
85 90 95

Phe Leu Phe Leu Gly Thr Leu Gly Leu Phe Gly Leu Thr Phe Ala 100 105 110

Phe Ile Ile Gln Glu Asp Glu Thr Ile Cys Ser Val Arg Arg Phe Leu 115 120 125

Trp Gly Val Leu Phe Ala Leu Cys Phe Ser Cys Leu Leu Ser Gln Ala 130 135 140

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Gln Leu Val Gly Leu Ala Leu Cys Leu Met Leu Val Gln Val Ile Ile 165 170 175

Ala Val Glu Trp Leu Val Leu Thr Val Leu Arg Asp Thr Arg Pro Ala 180 185 190

Cys Ala Tyr Glu Pro Met Asp Phe Val Met Ala Leu Ile Tyr Asp Met 195 200 205 Val Leu Leu Val Val Thr Leu Gly Leu Ala Leu Phe Thr Leu Cys Gly 210 215 220

Lys Phe Lys Arg Trp Lys Leu Asn Gly Ala Phe Leu Leu Ile Thr Ala 225 230 235 240

Phe Leu Ser Val Leu Ile Trp Val Ala Trp Met Thr Met Tyr Leu Phe 245 250 255

Gly Asn Val Lys Leu Gln Gln Gly Asp Ala Trp Asn Asp Pro Thr Leu 260 265 270

Ala Ile Thr Leu Ala Ala Ser Gly Trp Val Phe Val Ile Phe His Ala 275 280 285

Ile Pro Glu Ile His Cys Thr Leu Leu Pro Ala Leu Gln Glu Asn Thr 290 295 300

Pro Asn Tyr Phe Asp Thr Ser Gln Pro Arg Met Arg Glu Thr Ala Phe 305 310 315 320

Glu Glu Asp Val Gln Leu Pro Arg Ala Tyr Met Glu Asn Lys Ala Phe 325 330 335

Ser Met Asp Glu His Asn Ala Ala Leu Arg Thr Ala Gly Phe Pro Asn 340 345 350

Gly Ser Leu Gly Lys Arg Pro Ser Gly Ser Leu Gly Lys Arg Pro Ser 355 360 365

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- Cys Asp Leu Asp Ala Ile Trp Gly Ile Met Ala Ile His Lys Ala Leu $50 \hspace{1.5cm} 55 \hspace{1.5cm} 60 \hspace{1.5cm}$
- Val Met Cys Leu Gly Leu Pro Leu Phe Leu Phe Pro Gly Ala Trp Ala 65 70 75 80
- Gln Gly His Val Pro Pro Gly Cys Ser Gln Gly Leu Asn Pro Leu Tyr 85 90- 95
- Tyr Asn Leu Cys Asp Arg Ser Gly Ala Trp Gly Ile Val Leu Glu Ala 100 105 110
- Val Ala Gly Ala Gly Ile Val Thr Thr Phe Val Leu Thr Ile Ile Leu 115 120 125
- Val Ala Ser Leu Pro Phe Val Gln Asp Thr Lys Lys Arg Ser Leu Leu 130 135 140
- Gly Thr Gln Val Phe Phe Leu Leu Gly Thr Leu Gly Leu Phe Cys Leu 145 150 155 160
- Val Phe Ala Cys Val Val Lys Pro Asp Phe Ser Thr Cys Ala Ser Arg 165 170 175
- Arg Phe Leu Phe Gly Val Leu Phe Ala Ile Cys Phe Ser Cys Leu Ala 180 185 190
- Ala His Val Phe Ala Leu Asn Phe Leu Ala Arg Lys Asn His Gly Pro 195 200 205
- Arg Gly Trp Val Ile Phe Thr Val Ala Leu Leu Thr Leu Val Glu 210 215 220

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Ser	Pro	Cys	Ala 260	Val.	Ala	Asn	Met	Asp 265	Phe	Val	Met	Ala	Leu 270	Ile	Tyr
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Val	Ile	Pro 355	Glu	Val	Ser	Gln	Val 360	Thr	Lys	Ser	Ser	Pro 365	Glu	Gln	Ser
Tyr	Gln 370	Gly	Asp	Met	Tyr	Pro 375	Thr	Arg	Gly	Val	Gly 380	Tyr	Glu	Thr	Ile
Leu 385	Lys	Glu	Gln	Lys	Gly 390	Gln	Ser	Met	Phe	Val 395	Glu	Asn	Lys	Ala	Phe 400
Ser	Met	Asp	Glu	Pro 405	Val	Ala	Ala	Lys	Arg 410	Pro	Val	Ser	Pro	Tyr 415	Ser
Gly	Tyr	Asn	Gly 420	Gln	Leu	Leu	Thr	Ser 425	Val	Tyr	Gln	Pro	Thr 430	Glu	Met
Ala	Leu	Met 435	His	Lys	Val	Pro	Ser 440	Glu	Gly	Ala	Tyr	Asp 445	Ile	Ile	Leu

Pro Arg Ala Thr Ala Asn Ser Gln Val Met Gly Ser Ala Asn Ser Thr 450 455 460

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Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr 35 40 45

Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met 50 55 60

Leu Pro Thr Gln Phe Leu Phe Leu Cly Val Leu Gly Ile Phe Gly 65 70 75 80

Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr 85 90 95

Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu 100 105 110

Leu Ala His Ala Val Gly Leu Thr Lys Leu Val Arg Gly Arg Lys Pro 115 120 125

Leu Ser Leu Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val 130 135 140

Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr 145 150 155 Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Asn Glu Asp 165 170 Phe Val Leu Leu Thr Tyr Val Leu Phe Leu Met Ala Leu Thr Phe 180 Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg 195 200 His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp 210 215 Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Trp 230 235 240 Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe 245 Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg 260 265 Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu 280 Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu 295 Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys Asp Tyr Glu Val 345

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Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr 35 40 45

Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met 50 55 60

Leu Pro Thr Gln Phe Leu Phe Leu Gly Val Leu Gly Ile Phe Gly 65 70 75 80

Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr 85 90 95

Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu
100 105 110

Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Pro 115 120 125

Leu Ser Leu Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val 130 135 140

Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr 145 150 155 160

Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Asn Glu Asp 165 170 175

Phe Val Leu Leu Thr Tyr Val Leu Phe Leu Met Ala Leu Thr Phe 180 185 190

Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg

195 200 205

His Gly Ala His Ile Tyr Leu Thr Met Leu Ser Ile Ala Ile Trp 210 215 220

Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp 225 230 235 240

Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe 245 250 255

Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg
260 265 270

Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu 275 280 285

Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu 290 295 300

Ile Thr Arg Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr 305 310 315

Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser 325 330 335

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<400> 11

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<213> Bos taurus

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Ala Leu Gly Phe Ser Leu Val Gln Asp Ile Ile

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Val Lys Lys Glu Gly Ser

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Gly Asp Ser 50

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<213> Homo sapiens

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Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu 20 25 30

Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr 35 40 45

Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met 50 55 60

Leu Pro Thr Gln Phe Leu Phe Leu Gly Val Leu Gly Ile Phe Gly

Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr 85 90 95

Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu 100 105 110

Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Pro 115 120 125

Leu Ser Leu Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val 130 135 140

Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr 145 150 155 160

Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Arg Asn Glu Asp 165 170 175

Phe Val Leu Leu Leu Ala Tyr Val Leu Phe Leu Met Ala Leu Thr Phe 180 180 185

Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg 195 200 205

His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp 210 215 220

Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp 225 230 235 240

Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe 245 250 255

Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg 260 265 270

Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu 275 280 285

Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu 290 295 300

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Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser
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Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys Asp Tyr Glu Val
Lys Lys Glu Gly Ser
       355
<210> 18
<211> 2456
<212> DNA
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<220>
<223> RAI3 Polymorphic Allele Summary Sequence.
<220>
<221> misc feature
<222> (112)..(112)
<223> wherein "n" equals either G or A.
<220>
<221> misc_feature
<222> (364)..(364)
<223> wherein "n" equals either C or T.
<220>
<221> misc_feature
<222> (511)..(511)
<223> wherein "n" equals either C or T.
<220>
<221> misc_feature
<222> (523)..(523)
<223>
     wherein "n" equals either C or T.
<220>
<221> misc_feature
<222> (605)..(605)
<223> wherein "n" equals either A or G.
<220>
<221> misc_feature
<222> (797)..(797)
<223> wherein "n" equals either A or G.
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Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr

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<220>
<221> misc_feature
<222>
       (1111)..(1111)
<223> wherein "n" equals either T or C.
<220>
<221> misc feature
       (1173)..(1173)
       wherein "n" equals either A or G.
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tecttgteee tetgeteace cetegetegt teceteeete eggegaggge eneetttata
                                                                      120
acaactgctc agagtgcgag ggcgggatag ctgtccaagg tctcccccag cactgaggag
                                                                      180
ctegectget geeetettge gegegggaag cageaceaag tteaeggeea aegeettgge
                                                                      240
actagggtcc agaatggcta caacagtccc tgatggttgc cgcaatggcc tgaaatccaa
                                                                      300
gtactacaga ctttgtgata aggctgaagc ttggggcatc gtcctagaaa cggtggccac
                                                                      360
agenggggtt gtgacetegg tggeetteat geteactete eegateeteg tetgeaaggt
                                                                      420
gcaggactcc aacaggcgaa aaatgctgcc tactcagttt ctcttcctcc tgggtgtgtt
                                                                      480
gggcatcttt ggcctcacct tcgccttcat natcggactg gangggagca cagggcccac
                                                                      540
acgettette etetttggga teetetttte catetgette teetgeetge tggeteatge
                                                                      600
tgtcngtctg accaagctcg tccgggggag gaagcccctt tccctgttgg tgattctggg
                                                                      660
tetggeegtg ggetteagee tagteeagga tgttateget attgaatata ttgteetgae
                                                                      720
catgaatagg accaacgtca atgtcttttc tgagctttcc gctcctcgtc gcaatgaaga
                                                                      780
ctttgtcctc ctgctcncct acgtcctctt cttgatggcg ctgaccttcc tcatgtcctc
                                                                      840
                                                                      900
etteacette tgtggtteet teaegggetg gaagagaeat ggggeeeaca tetaeeteae
gatgeteete teeattgeea tetgggtgge etggateace etgeteatge tteetgaett
                                                                      960
tgaccgcagg tgggatgaca ccatcctcag ctccgccttg gctgccaatg gctgggtgtt
                                                                     1020
                                                                     1080
cctgttggct tatgttagtc ccgagttttg gctgctcaca aagcaacgaa accccatgga
ttatcctgtt gaggatgctt tctgtaaacc ncaactcgtg aagaagagct atggtgtgga
                                                                     1140
gaacagagcc tactctcaag aggaaatcac tcnaggtttt gaagagacag gggacacgct
                                                                     1200
ctatgccccc tattccacac attttcagct gcagaaccag cctccccaaa aggaattctc
                                                                     1260
catcccacgg gcccacgctt ggccgagccc ttacaaagac tatgaagtaa agaaagaggg
                                                                     1320
cagctaactc tgtcctgaag agtgggacaa atgcagccgg gcggcagatc tagcgggagc
                                                                     1380
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tcaaagggat gtgggcgaaa tcttgagtct tctgagaaaa ctgtacaaga cactacggga
                                                                    1440
acagtttgcc tccctcccaq cctcaaccac aattcttcca tgctgqgct qatgtgqqct
                                                                    1500
agtaagactc cagttettag aggegetgta gtatttttt ttttttgtet cateetttgg
                                                                    1560
atacttettt taagtgggag teteaggeaa eteaagttta gaeeettaet etttttgttt
                                                                    1620
gttttttgaa acaggatctt gctctgtcac ccaggcttga gtgcagtggt gcgatcacag
                                                                    1680
cccagtgcag cctcgaccac ctgtgctcaa gcaatcctcc catctccatc tcccaaagtg
                                                                    1740
ctgggatgac aggcgtgagc cacagctccc agcctaggcc cttaatcttg ctgttatttt
                                                                    1800
ccatggacta aaggtetggt catetgaget cacgetgget cacacagete taggggeetg
                                                                    1860
                                                                    1920
ctcctctaac tcacagtggg ttttgtgagg ctctgtggcc cagagcagac ctgcatatct
gagcaaaaat agcaaaagcc tctctcagcc cactggcctg aatctacact ggaagccaac
                                                                    1980
ttgctggcac ccccgctccc caacccttct tgcctgggta ggagaggcta aagatcaccc
                                                                    2040
taaatttact catctctcta gtgctgcctc acattgggcc tcagcagctc cccagcacca
                                                                    2100
attcacaggt cacccctctc ttcttgcact gtccccaaac ttgctgtcaa ttccgagatc
                                                                    2160
taatctcccc ctacgctctg ccaggaattc tttcagacct cactagcaca agcccggttg
                                                                    2220
ctccttgtca ggagaatttg tagatcattc tcacttcaaa ttcctggggc tgatacttct
                                                                    2280
ctcatcttgc accccaacct ctgtaaatag atttaccgca tttacggctg cattctgtaa
                                                                    2340
gtgggcatgg tctcctaatg gaggagtgtt cattgtataa taagttattc acctgagtat
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gcaataaaga tgtggtggcc actctttcat ggtggtggca gcaaaaaaaa aaaaaa
                                                                    2456
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<210> 19
<211> 357
<212> PRT
<213> Artificial Sequence
<220>
<223> RAI3 Polymorphic Allele Summary Sequence.

<220>
<221> MISC_FEATURE
<222> (118)..(118)
<223> wherein "Xaa" equals either 'Ser' or 'Gly'.

<220>
<221> MISC_FEATURE
<222> (182)..(182)
<223> wherein "Xaa" equals either 'Thr' or 'Ala'.
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<220>

- <221> MISC FEATURE
- <222> (307)..(307)
- <223> wherein "Xaa" equals either 'Gln' or 'Arg'.

<400> 19

Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys

1 10 15

Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu 20 25 30

Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr 35 40 45

Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met 50 60

Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly 65 70 75 80

Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr 85 90 95

Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu 100 105 110

Leu Ala His Ala Val Xaa Leu Thr Lys Leu Val Arg Gly Arg Lys Pro 115 120 125

Leu Ser Leu Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val 130 135 140

Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr 145 150 155 160

Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Arg Asn Glu Asp 165 170 175

Phe Val Leu Leu Leu Xaa Tyr Val Leu Phe Leu Met Ala Leu Thr Phe 180 185 190

Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg 195 200 205 His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp 210 215 220

Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp 225 230 235 240

Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe 245 250 255

Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg
260 265 270

Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu 275 280 285

Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu 290 295 300

Ile Thr Xaa Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr 305 310 315 320

Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser 325 $^{\circ}$ 330 335

Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys Asp Tyr Glu Val 340 345 350

Lys Lys Glu Gly Ser 355

<210> 20

<211> 357

<212> PRT

<213> Homo sapiens

<400> 20

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Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu
20 25 30

Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr

35 40 45

- Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met 50 55 60
- Leu Pro Thr Gln Phe Leu Phe Leu Leu Gly Val Leu Gly Ile Phe Gly 65 70 75 80
- Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr 85 90 95
- Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu 100 105 110
- Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Pro 115 120 125
- Leu Ser Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val
 130 135 140
- Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr 145 150 155 160
- Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Arg Asn Glu Asp 165 170 175
- Phe Val Leu Leu Thr Tyr Val Leu Phe Leu Met Ala Leu Thr Phe 180 185 190
- Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg 195 200 205
- His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp 210 215 220
- Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp 225 230 235 240
- Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe 245 250 255
- Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg 260 265 270

Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu 275 280 285

Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu 290 295 300

Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr 305 310 315 320

Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser 325 330 335

Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys Asp Tyr Glu Val 340 345 350

Lys Lys Glu Gly Ser 355

<210> 21

<211> 357

<212> PRT

<213> Homo sapiens

<400> 21

Met Ala Thr Thr Val Pro Asp Gly Cys Arg Asn Gly Leu Lys Ser Lys

1 10 15

Tyr Tyr Arg Leu Cys Asp Lys Ala Glu Ala Trp Gly Ile Val Leu Glu 20 25 30

Thr Val Ala Thr Ala Gly Val Val Thr Ser Val Ala Phe Met Leu Thr 35 40 45

Leu Pro Ile Leu Val Cys Lys Val Gln Asp Ser Asn Arg Arg Lys Met 50 55 60

Leu Pro Thr Gln Phe Leu Phe Leu Gly Val Leu Gly Ile Phe Gly 65 70 75 80

Leu Thr Phe Ala Phe Ile Ile Gly Leu Asp Gly Ser Thr Gly Pro Thr 85 90 95

Arg Phe Phe Leu Phe Gly Ile Leu Phe Ser Ile Cys Phe Ser Cys Leu Leu Ala His Ala Val Ser Leu Thr Lys Leu Val Arg Gly Arg Lys Pro Leu Ser Leu Leu Val Ile Leu Gly Leu Ala Val Gly Phe Ser Leu Val Gln Asp Val Ile Ala Ile Glu Tyr Ile Val Leu Thr Met Asn Arg Thr · Asn Val Asn Val Phe Ser Glu Leu Ser Ala Pro Arg Arg Asn Glu Asp Phe Val Leu Leu Thr Tyr Val Leu Phe Leu Met Ala Leu Thr Phe Leu Met Ser Ser Phe Thr Phe Cys Gly Ser Phe Thr Gly Trp Lys Arg His Gly Ala His Ile Tyr Leu Thr Met Leu Leu Ser Ile Ala Ile Trp Val Ala Trp Ile Thr Leu Leu Met Leu Pro Asp Phe Asp Arg Arg Trp Asp Asp Thr Ile Leu Ser Ser Ala Leu Ala Ala Asn Gly Trp Val Phe Leu Leu Ala Tyr Val Ser Pro Glu Phe Trp Leu Leu Thr Lys Gln Arg Asn Pro Met Asp Tyr Pro Val Glu Asp Ala Phe Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Glu Asn Arg Ala Tyr Ser Gln Glu Glu Ile Thr Gln Gly Phe Glu Glu Thr Gly Asp Thr Leu Tyr Ala Pro Tyr Ser Thr His Phe Gln Leu Gln Asn Gln Pro Pro Gln Lys Glu Phe Ser

325 330 335

Ile Pro Arg Ala His Ala Trp Pro Ser Pro Tyr Lys Asp Tyr Glu Val 345 Lys Lys Glu Gly Ser 355 <210> 22 <211> 40 <212> DNA <213> Homo sapiens <400> 22 40 ctagaaacgg tggccacagc cggggttgtg acctcggtgg <210> 23 <211> 40 <212> DNA <213> Homo sapiens <400> 23 40 ctagaaacgg tggccacagc tggggttgtg acctcggtgg <210> 24 <211> 44 <212> DNA <213> Homo sapiens <400> 24 44 tgcctgctgg ctcatgctgt cagtctgacc aagctcgtcc gggg <210> 25 <211> 44 <212> DNA <213> Homo sapiens <400> 25 44 tgcctgctgg ctcatgctgt cggtctgacc aagctcgtcc gggg <210> 26 <211> 50 <212> DNA <213> Homo sapiens <400> 26 50

<210> 27

tcctgttgag gatgctttct gtaaacctca actcgtgaag aagagctatg

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<213> Homo sapiens
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<210> 28
<211> 40
<212> DNA
<213> Homo sapiens
<400> 28
                                                                    40
tctcaagagg aaatcactca aggttttgaa gagacagggg
<210> 29
<211> 40
<212> DNA
<213> Homo sapiens
<400> 29
                                                                    40
tctcaagagg aaatcactcg aggttttgaa gagacagggg
<210> 30
<211> 42
<212> DNA
<213> Homo sapiens
<400> 30
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gcccacgctt ggccgagccc ttacaaagac tatgaagtaa ag
<210> 31
<211> 17
<212> DNA
<213> Homo sapiens
<400> 31
                                                                    17
gcccacgctt ggccgag
<210> 32
<211> 19
<212> DNA
<213> Homo sapiens
<400> 32
                                                                    19
ctttacttca tagtctttg
<210> 33
<211> 42
<212> DNA
<213> Artificial Sequence
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<220>
<223> Degenerate Oligonucleotide.
<220>
<221> misc_feature
<222>
      (3)..(39)
<223> wherein "n" equals A, C, G, or T.
<220>
<221> misc_feature
<222>
      (6)..(33)
<223> wherein "y" equals C, or T.
<220>
<221> misc feature
<222>
      (27)..(42)
<223>
      wherein "r" equals A, or G.
<400> 33
                                                                       42
geneaygent ggeentence ntayaargay taygargtna ar
<210>
       34
<211>
       17
<212>
       DNA
<213>
      Artificial Sequence
<220>
<223> Degenerate Oligonucleotide.
<220>
<221> misc_feature
<222>
      (3)..(15)
<223> wherein "n" equals A, C, G, or T.
<220>
      misc_feature
<221>
<222>
       (6)..(6)
       wherein "y" equals C, or T.
<223>
<400> 34
gcncaygcnt ggccntc
                                                                       17
<210>
       35
<211>
       23
<212>
      DNA
<213>
      Artificial Sequence
<220>
      Degenerate Oligonucleotide.
<223>
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<220>

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<221> misc_feature
<222>
      (1)..(16)
<223> wherein "y" equals C, or T.
<220>
<221> misc_feature
<222> (4)..(22)
<223> wherein "n" equals A, C, G, or T.
<220>
<221> misc_feature
<222> (10)..(19)
<223> wherein "r" equals A, or G.
<400> 35
                                                                      23
yttnacytcr tartcyttrt ang
<210> 36
<211> 38
<212> DNA
<213> Homo sapiens
<400> 36
                                                                      38
gcgcggccca attgcatggc tacaacagtc cctgatgg
<210> 37
<211>
      33′
<212>
      DNA
<213> Homo sapiens
<400> 37
geggeeeteg agttagetge cetettett tac
                                                                      33
<210> 38
<211>
       16
<212>
      PRT
<213> Homo sapiens
<400> 38
Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Val Phe Ala
<210>
      39
<211>
      11
<212>
      PRT
<213> Bacteriophage T7
<400> 39
Asp Tyr Lys Asp Asp Asp Asp Ala Arg Asn Ser
                5
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<211>
      27
<212> PRT
<213> Homo sapiens
<400> 40
Met Lys Thr Ile Ile Ala Leu Ser Tyr Ile Phe Cys Leu Val Phe Ala
Asp Tyr Lys Asp Asp Asp Asp Ala Arg Asn Ser
           20
<210> 41
<211>
      39
<212>
      DNA
<213> Homo sapiens
<400> 41
gcggccagat ctgccaccat ggctacaaca gtccctgat
                                                                    39
<210> 42
<211> 60
<212>
      DNA
<213> Homo sapiens
<400> 42
geggeeeteg agetaettgt egtegtegte ettgtagtee atgetgeeet etttettae
                                                                    60
<210>
      43
<211>
      9
<212> PRT
<213> Homo sapiens
<400> 43
Met Asp Tyr Lys Asp Asp Asp Lys
               5
<210> 44
<211> 55
<212> DNA
<213> Homo sapiens
<400> 44
egggatecta ettgtegteg tegteettgt agtegetgee etetttettt aette
<210>
      45
<211>
      21
<212> DNA
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<210> 40

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<213> Homo sapiens
  <400> 45
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  <211> 22
  <212> DNA
 <213> Homo sapiens
 <400> 46
                                                                      22
 gtgggatgga gaattccttt tg
 <210> 47
 <211> 22
 <212> DNA
 <213> Homo sapiens
 <400> 47
                                                                      22
 attccacaca ttttcagctg ca
 <210> 48
 <211> 21
 <212> DNA
 <213> Homo sapiens
 <400> 48
                                                                      21
 ggatggagaa ttccttttgg g
 <210> 49
 <211> 25
 <212> PRT
 <213> Homo sapiens
 <400> 49
 Cys Leu Thr Met Asn Arg Thr Asn Val Asn Val Phe Ser Glu Leu Ser
, Ala Pro Arg Arg Asn Glu Asp Phe Val
            20
 <210> 50
 <211> 18
 <212> PRT
 <213> Homo sapiens
 <400> 50
 Cys Met Leu Pro Asp Phe Asp Arg Trp Asp Asp Thr Thr Leu Ser
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<210> 51 <211> 21 <212> PRT <213> Homo sapiens <400> 51 Cys Lys Pro Gln Leu Val Lys Lys Ser Tyr Gly Val Asn Glu Arg Ala 10 Tyr Ser Gln Glu Glu 20 <210> 52 <211> 26 <212> DNA <213> Artificial Sequence <220> Synthesized Antisense Oligonucleotide. <223> <400> 52 26 uuccaguucc acggcacuuc augcuu <210> 53 <211> 26 <212> DNA <213> Artificial Sequence <220> Synthesized Antisense Oligonucleotide. <223> <400> 53 26 guccaguccg augaugaagg cgaagu <210> 54 <211> 26 <212> DNA <213> Artificial Sequence

Ser Ala

<223>

<400> 54

caguuguuau aaaggcggcc cucgcu

26

Synthesized Antisense Oligonucleotide.

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<210> 55
<211>
      26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthesized Antisense Oligonucleotide.
<400> 55
uuguagccau ucuggacccu agugcu
                                                                     26
<210> 56
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthesized Antisense Oligonucleotide.
<400> 56
ucuuccagcc cgugaaggaa ccacau
                                                                     26
<210> 57
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthesized Antisense Oligonucleotide.
<400> 57
accuugaccu uauccgcaca ggagau
                                                                     26
<210> 58
<211>
      26
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthesized Antisense Oligonucleotide.
<400> 58
gagccucccc gggaauauug uugacu
                                                                     26
<210> 59
<211>
      26
<212> DNA
<213>
      Artificial Sequence
<220>
      Synthesized Antisense Oligonucleotide.
<223>
<400> 59
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gcugau	cca ggucuuaccg auguuu	26
<210>	60	
<211>	25	
<212>		
<213>	Artificial Sequence	
<220>	·	
<223>	Synthesized Antisense Oligonucleotide.	
<400>	60	25
acacca	agga agugeeegae euueu	25
<210>		
<211> <212>	26 DNA	
<213>		
72137	· ·	
<220>		
<223>	Synthesized Antisense Oligonucleotide.	
<400>	61	
gacugaa	aacu ggeguecace cuacuu	26
<210>	62	
	24	
<212>	DNA	
<213>	Homo sapiens	
<400>	62	
	gagg agagctatga caca	24
<210>	63	
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	gcac tcataacgtc ag	22
	•	
<210>	64	
<211>	29	
<212>	DNA	
<213>	Homo sapiens	
<400>	64	
	acag tcatcatagg gcagctcgt	29
<210>	65	
<211>	41	

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<213> Homo sapiens
<220>
<221> misc_feature
<222> (21)..(21)
<223> wherein "n" equals either C, or T.
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ctgagcagtt gttataaagg nggccctcgc cggagggagg g
                                                                               41
<210> 66
<211> 41
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (21)..(21)
<223> wherein "n" equals either T, or C.
<400> 66
                                                                               41
gccccagcgc tctgggctcc nggcgcctca cttaccctag t
<210> 67
<211> 41
<212> DNA
<213> Homo sapiens
<220>
<221> misc feature
<222> (21)..(21)
<223> wherein "n" equals either G, or A.
<400> 67
gccaccgagg tcacaacccc ngctgtggcc accgtttcta g
                                                                               41
<210> 68
<211> 41
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (21)..(21)
<223> wherein "n" equals either G, or A.
<400> 68
gtgctcccgt ccagtccgat natgaaggcg aaggtgaggc c
                                                                               41
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<210> 69
<211> 41
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222>
      (21)..(21)
<223> wherein "n" equals either G, or A.
<400> 69
                                                                     41
cgtgtgggcc ctgtgctccc ntccagtccg atgatgaagg c
<210> 70
<211> 41
<212> DNA
<213> Homo sapiens
<220>
<221> misc_feature
<222> (21)..(21)
<223> wherein "n" equals either T, or C.
<400> 70
                                                                     41
catcaagaag aggacgtagg ngagcaggag gacaaagtct t
<210> 71
<211>
      39
<212> DNA
<213> Homo sapiens
<400> 71
                                                                     39
tgtaaaacga cggccagtgt cagacggttt ttgggtcat
<210> 72
<211> 39
<212> DNA
<213> Homo sapiens
<400> 72
                                                                     39
tgtaaaacga cggccagtgt cagacggttt ttgggtcat
<210>
      73
<211>
      39
<212> DNA
<213>
      Homo sapiens
<400> 73
                                                                     39
tgtaaaacga cggccagtaa taccttctcc ccactccaa
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<210>	74				
<211>	39				
<212>	DNA				
<213>	Homo sapiens				
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